



results of BLAST

BLASTP 2.2.4 [Aug-26-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1035909885-07974-2763

Query=

(512 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

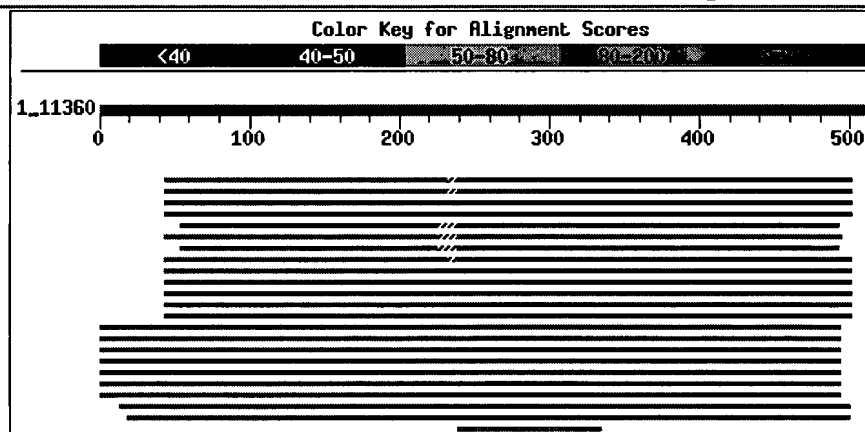
1,226,480 sequences; 390,314,779 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 662 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:		Score (bits)	E Value	
gi 337938 gb AAA64297.1	(M73240) hepatocyte growth factor ...	548	e-155	L
gi 20542440 ref XP_168542.1	(XM_168542) similar to Hepatoc...	542	e-153	L
gi 226566 prf 1602237A	hepatocyte growth factor [Rattus no...	535	e-151	
gi 87647 pir S06794	hepatocyte growth factor precursor (ve...	535	e-151	
gi 18490837 gb AAH22308.1	(BC022308) Similar to hepatocyte...	514	e-144	L
gi 2135339 pir I59214	hepatocyte growth factor short form ...	509	e-143	
gi 184030 gb AAA35980.1	(M77227) competitive HGF antagonis...	509	e-143	L
gi 12583697 dbj BAB21499.1	(AB046610) hepatocyte growth fa...	506	e-142	

gi 220438 dbj BAA01065.1	(D10213) hepatocyte growth factor...	493	e-138	L
gi 433431 emb CAA51054.1	(X72307) hepatocyte growth factor...	488	e-137	L
gi 8393526 ref NP_058713.1	(NM_017017) hepatocyte growth f...	488	e-137	L
gi 632774 gb AAB31855.1	(S71816) hepatocyte growth factor;...	487	e-136	L
gi 20822586 ref XP_131908.1	(XM_131908) similar to hepatoc...	487	e-136	L
gi 1311661 gb AAC50471.1	(U37055) hepatocyte growth factor...	485	e-136	L
gi 10337615 ref NP_066278.1	(NM_020998) macrophage stimula...	485	e-136	L
gi 123114 sp P26927 HGFL HUMAN	Hepatocyte growth factor-lik...	482	e-135	
gi 90615 pir A40332	macrophage-stimulating protein 1 precu...	412	e-114	
gi 14714805 gb AAH10551.1	(BC010551) hepatocyte growth fac...	412	e-114	L
gi 6680215 ref NP_032269.1	(NM_008243) hepatocyte growth f...	410	e-113	L
gi 13242239 ref NP_077328.1	(NM_024352) macrophage stimula...	408	e-113	L
gi 1130680 emb CAA58864.1	(X84045) hepatocyte growth facto...	405	e-112	
gi 1141775 gb AAC63092.1	(U28054) hepatocyte growth factor...	403	e-111	
gi 2134350 pir I51285	hepatocyte growth factor/scatter fac...	398	e-109	
gi 1419544 emb CAA56430.1	(X80131) HGF/SF [Gallus gallus]	398	e-109	
gi 2134190 pir I51283	hepatocyte growth factor precursor -...	386	e-106	
gi 1095779 prf I2109382A	hepatocyte growth factor [Xenopus ...	386	e-106	
gi 4389172 pdb 1NK1 A	Chain A, Nk1 Fragment Of Human Hepato...	346	4e-94	
gi 1378042 gb AAC50539.1	(U46010) HGF agonist/antagonist [...	345	8e-94	L
gi 12394255 gb AAG53459.1	(M75984) hepatocyte growth facto...	345	8e-94	
gi 16975412 pdb 1GMO C	Chain C, Crystal Structures Of Nk1-H...	345	1e-93	
gi 3891529 pdb 1BHT A	Chain A, Nk1 Fragment Of Human Hepato...	340	3e-92	
gi 17942663 pdb 1GP9 C	Chain C, A New Crystal Form Of The N...	333	3e-90	
gi 11544434 emb CAC17639.1	(AL137798) dJ1182A14.3 (similar...	317	3e-85	
gi 16758216 ref NP_445943.1	(NM_053491) plasminogen [Rattu...	314	2e-84	L
gi 2921762 gb AAC40051.1	(AF042856) hepatocyte growth fact...	311	1e-83	L
gi 2305256 gb AAB65760.1	(AF012297) plasminogen [Macropus ...	306	4e-82	
gi 1130676 emb CAA58862.1	(X84043) hepatocyte growth facto...	294	3e-78	
gi 11399751 gb AAB52574.1	(U57455) growth factor Livertine ...	281	2e-74	
gi 1619621 emb CAA69989.1	(Y08734) hepatocyte growth facto...	275	1e-72	
gi 7512243 pir T18518	apolipoprotein(a) - western European...	261	2e-68	
gi 114063 sp P14417 APOA MACMU	Apolipoprotein(a) (Apo(a)) (...	258	2e-67	
gi 5031885 ref NP_005568.1	(NM_005577) lipoprotein, Lp(a);...	253	6e-66	L
gi 225794 prf I313352A	apolipoprotein a [Homo sapiens]	253	6e-66	
gi 23308677 ref NP_694512.1	(NM_152980) macrophage stimula...	229	6e-59	L
gi 130319 sp P06867 PLMN PIG	Plasminogen >gi 2144494 pir P...	206	7e-52	
gi 1806583 gb AAC48717.1	(U33171) plasminogen [Erinaceus e...	205	2e-51	
gi 6708459 gb AAF25945.1	AF213397_1 (AF213397) hepatocyte g...	204	2e-51	
gi 2499860 sp Q29485 PLMN ERIEU	Plasminogen precursor >gi 2...	204	2e-51	
gi 2507247 sp P06868 PLMN BOVIN	Plasminogen precursor >gi 1...	203	4e-51	
gi 15928602 gb AAH14773.1	(BC014773) plasminogen [Mus musc...	202	9e-51	L
gi 6679381 ref NP_032903.1	(NM_008877) plasminogen [Mus mu...	200	3e-50	L
gi 190026 gb AAA36451.1	(M74220) plasminogen [Homo sapiens]	199	1e-49	L
gi 4505881 ref NP_000292.1	(NM_000301) plasminogen [Homo s...	199	1e-49	L
gi 625234 pir PLHU	plasmin (EC 3.4.21.7) precursor [valida...	199	1e-49	
gi 130317 sp P12545 PLMN MACMU	Plasminogen precursor >gi 86...	198	2e-49	
gi 3318760 pdb 2HGF	Hairpin Loop Containing Domain Of Hep...	196	5e-49	
gi 18139619 gb AAL58519.1	(AY069985) plasminogen [Canis fa...	179	8e-44	
gi 21465835 pdb 1KI0 A	Chain A, The X-Ray Structure Of Huma...	165	1e-39	
gi 2118100 pir A61545	plasmin (EC 3.4.21.7) precursor - ho...	155	9e-37	
gi 13161395 dbj BAB33031.1	(AB056447) hepatocyte growth fa...	150	6e-35	
gi 2118101 pir B61545	plasmin (EC 3.4.21.7) precursor - sh...	148	2e-34	
gi 2815616 gb AAB97886.1	(AF029691) apolipoprotein a [Papi...	145	2e-33	
gi 387031 gb AAA60124.1	(K02922) plasminogen [Homo sapiens]	137	3e-31	
gi 12394256 gb AAG53460.1	(M75984) hepatocyte growth facto...	134	2e-30	
gi 135806 sp P00735 THRB BOVIN	Prothrombin precursor >gi 62...	119	7e-26	
gi 163755 gb AAA30781.1	(J00041) preprothrombin [Bos taurus]	118	2e-25	
gi 2653563 dbj BAA23643.1	(D63779) HGF alpha-chain [Gallus...	115	2e-24	
gi 6683108 dbj BAA89046.1	(AB028871) prothrombin [Struthio...	107	3e-22	
gi 4503635 ref NP_000497.1	(NM_000506) coagulation factor ...	107	4e-22	L
gi 1335344 emb CAA23842.1	(V00595) prothrombin [Homo sapiens]	107	5e-22	L

gi 6753798 ref NP_034298.1	(NM_010168) coagulation factor ...	106	8e-22	L
gi 289825 gb AAA21619.1	(M81391) thrombin [Gallus gallus]	104	3e-21	
gi 266801 sp Q01177 PLMN RAT	Plasminogen >gi 321331 pir A4...	103	6e-21	
gi 12621076 ref NP_075213.1	(NM_022924) coagulation factor...	102	1e-20	L
gi 5921269 emb CAB56422.1	(AJ011396) hepatocyte growth fac...	102	1e-20	
gi 13346502 ref NP_077818.1	(NM_024492) apolipoprotein(a) ...	100	4e-20	L
gi 627678 pir E61545	plasmin (EC 3.4.21.7) precursor - dog...	100	9e-20	
gi 22831326 dbj BAC16209.1	(AB087137) receptor tyrosine ki...	99	1e-19	
gi 6103600 gb AAF03680.1	(AF158663) apolipoprotein(a) [Hom...	99	2e-19	
gi 627772 pir C61545	plasmin (EC 3.4.21.7) precursor - goa...	98	3e-19	
gi 15825918 pdb 1I5K B	Chain B, Structure And Binding Deter...	96	1e-18	
gi 22773778 gb AAN05008.1	(AY143173) muscle-specific recep...	96	1e-18	
gi 422541 pir A47299	ror-related receptor RTK - Pacific el...	94	4e-18	
gi 14702169 ref NP_127509.1	(NM_033011) plasminogen activa...	94	4e-18	L
gi 4505861 ref NP_000921.1	(NM_000930) plasminogen activat...	94	5e-18	L
gi 339834 gb AAB59510.1	(L00153) plasminogen activator [Ho...	94	5e-18	L
gi 1079221 pir S33879	plasmin precursor - lamprey (fragments)	93	8e-18	
gi 5107603 pdb 1KIV	Recombinant Kringle Iv-10M66 VARIANT ...	93	8e-18	
gi 441174 dbj BAA00881.1	(D01096) tissue plasminogen activ...	93	9e-18	L
gi 21730366 pdb 1JFN A	Chain A, Solution Structure Of Human...	92	1e-17	
gi 5107746 pdb 3KIV	Recombinant Kringle Iv-10M66 VARIANT ...	92	2e-17	
gi 6573460 pdb 1B2I A	Chain A, Kringle 2 Domain Of Human Pl...	92	2e-17	
gi 6103599 gb AAF03679.1	(AF158663) apolipoprotein(a) [Hom...	92	2e-17	
gi 280728 pir A60140	plasmin (EC 3.4.21.7) precursor - chi...	92	2e-17	
gi 2815618 gb AAB97887.1	(AF029692) plasminogen [Papio ham...	92	2e-17	
gi 9989696 gb AAG01184.2	(AF294796) ROR2 protein [Homo sap...	92	2e-17	
gi 13878706 sp Q01974 ROR2 HUMAN	Tyrosine-protein kinase tr...	92	2e-17	
gi 19743898 ref NP_004551.2	(NM_004560) receptor tyrosine ...	92	2e-17	L
gi 6103598 gb AAF03678.1	(AF158663) apolipoprotein(a) [Hom...	92	2e-17	
gi 6103597 gb AAF03677.1	(AF158663) apolipoprotein(a) [Hom...	91	3e-17	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|337938|gb|AAA64297.1| (M73240) hepatocyte growth factor [Homo sapiens]
gi|3845413|gb|AAC71655.1| (AC004960) hepatocyte growth factor [Homo sapiens]
Length = 723

Score = 548 bits (1412), Expect = e-155
Identities = 263/263 (100%), Positives = 263/263 (100%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 299
QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
Sbjct: 32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Query: 300 ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
Sbjct: 92 ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVECMT CNG 419
WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVECMT CNG
Sbjct: 152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVECMT CNG 211

Query: 420 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 479
ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
Sbjct: 212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Query: 480 HTRWEYCAIKTCADNTMNDTDVP 502
HTRWEYCAIKTCADNTMNDTDVP
Sbjct: 272 HTRWEYCAIKTCADNTMNDTDVP 294

Score = 201 bits (510), Expect = 3e-50

Identities = 88/173 (50%), Positives = 115/173 (65%), Gaps = 3/173 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENF 114
E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H Y L+EN+
Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYRG---KDLQENY 171

Query: 115 CRNPDGDPGGPWCYTTPDAVRFQSCGIKSCREAACVWCNGEYRGAVDRTESGRECNRWD 174
CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C RWD
Sbjct: 172 CRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWD 231

Query: 175 LNHPHNHPFEPGKFLDNLDDNYCRNPDGSRPWCYTTPDNIEREFCDLPRCG 227
PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
Sbjct: 232 HQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRWCYTLDPHTRWEYCAIKTCA 284

Score = 152 bits (385), Expect = 9e-36

Identities = 84/201 (41%), Positives = 105/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDH 100
GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
Sbjct: 181 GPWCFTSNPEVRYEVCDDIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 238

Query: 101 KYTPTL--RNGLEENFCRNPDGDPGGPWCYTTPDAVRFQSCGIKSCRE----- 146
K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+C +
Sbjct: 239 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLET 297

Query: 147 AACVWCNGEYRGAVDRTESGRECNRWDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSR 206
C+ GE YRG V+ +G C RWD +PH H P F L +NYCRNPDGSE
Sbjct: 298 TECIQQGEGYRGTVNTIWNIGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSES 357

Query: 207 PWCYTTPDNIEREFCD-LPRC 226
PWC+TTDPNI +C +P C
Sbjct: 358 PWCFTTDPNIRVGYSQIPNC 378

Score = 139 bits (351), Expect = 7e-32

Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRNPRGEEGGP 390
C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
Sbjct: 206 CMTCNESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 264

Query: 391 WCFTSNPEVRYEVCDDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
WC+T +P R+E C I C++ EC+ GE YRG ++ +G CQRW
Sbjct: 265 WCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGGEGYRGTVNTIWNIGIPCQRW 324

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
D Q PH H PE + K +NYCRNPDG PWC+T DP+ R YC+
Sbjct: 325 DSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYS 373

Score = 135 bits (341), Expect = 1e-30

Identities = 77/173 (44%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGP 390
CI G+G Y+GTV+ +GI CQ W S PHEH +++ KDL+ENYCRNP G E P
Sbjct: 300 CIQGGEGYRGTVNTIWNIGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSE-SP 358

Query: 391 WCFTSNPEVRYEVCDDIPQCSEV---ECMTCNGESYRGLMDHTESGKICQRWDHQTP--H 444
WCFT++P +R C IP C +C NG++Y G + T SG C WD H
Sbjct: 359 WCFTTDPNIRVGYSQIPNCDMSHGQDCYRGNNGKNYMGNLSQTRSGLTCSMWDKNMEDLH 418

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD ++NYCRNPD PWCYT +P W+YC I C +T
 Sbjct: 419 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 468

Score = 128 bits (322), Expect = 2e-28
 Identities = 75/175 (42%), Positives = 99/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRG+ T G+PCQ W ++P++H TP L EN+CRNPDG P
 Sbjct: 300 CIQQGGEGYRGTVNTIWNIGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDPGSE-SP 358

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA---CVWCNGEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ WD N H
 Sbjct: 359 WCFTTDPNIRVGYSQIPNCDMSHGQDCYRGNKGNYMGNLSQTRSGLTCSMWDKNMEDLH 418

Query: 180 NHPPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTPNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 419 RHIFWEPDA---SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 470

☐ >gi|20542440|ref|XP_168542.1| (XM_168542) similar to Hepatocyte growth factor p
 factor) (SF) (Hepatopoeitin A) [Homo sapiens]
 gi|123116|sp|P14210|HGF_HUMAN Hepatocyte growth factor precursor (Scatter factor)
 (Hepatopoeitin A)
 gi|87648|pir|JH0579 hepatocyte growth factor precursor - human
 gi|184032|gb|AAA52648.1| (M60718) hepatocyte growth factor [Homo sapiens]
 gi|219700|dbj|BAA14348.1| (D90334) hepatocyte growth factor [Homo sapiens]
 gi|306846|gb|AAA52650.1| (M29145) hepatocyte growth factor [Homo sapiens]
 gi|337936|gb|AAA64239.1| (M73239) hepatocyte growth factor [Homo sapiens]
 Length = 728

Score = 542 bits (1396), Expect = e-153
 Identities = 263/268 (98%), Positives = 263/268 (98%), Gaps = 5/268 (1%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 299
 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
 Sbjct: 32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Query: 300 ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
 Sbjct: 92 ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVEC 414
 WSSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVEC
 Sbjct: 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVEC 211

Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWC 474
 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWC
 Sbjct: 212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWC 271

Query: 475 YTLDPHTRWEYCAIKTCADNTMNDTDVP 502
 YTLDPHTRWEYCAIKTCADNTMNDTDVP
 Sbjct: 272 YTLDPHTRWEYCAIKTCADNTMNDTDVP 299

Score = 205 bits (521), Expect = 2e-51
 Identities = 89/175 (50%), Positives = 118/175 (66%), Gaps = 2/175 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E
 Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPGDPGGPWCYTTPAVRFQSCGIKSCREAAACVWCNGEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R
 Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSRPWCYTTPDNIEREFCDLPRCG 227
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCA 289

Score = 152 bits (385), Expect = 9e-36
 Identities = 84/201 (41%), Positives = 105/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
 Sbjct: 186 GPWCFTSNPEVRYEVCDDIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCYTTPDAVRFQSCGIKSCRE----- 146
 K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+C +
 Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLET 302

Query: 147 AACVWCNGEYRGAVDRTESGRECNRWDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSR 206
 C+ GE YRG V+ +G C RWD +PH H P F L +NYCRNPDGSE
 Sbjct: 303 TECIQQGEGYRGTVNTIWNIGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSES 362

Query: 207 PWCYTTPDNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P C
 Sbjct: 363 PWCFTTDPNIRVGYSQIPNC 383

Score = 139 bits (351), Expect = 7e-32
 Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
 Sbjct: 211 CMTTCNGESYRGLMDHTESGKICQRWDHQTTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 269

Query: 391 WCFTSNPEVRYEVCDDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
 WC+T +P R+E C I C++ EC+ GE YRG ++ +G CQRW
 Sbjct: 270 WCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQQGEGYRGTVNTIWNIGIPCQRW 329

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
 D Q PH H PE + K +NYCRNPDG PWC+T DP+ R YC+
 Sbjct: 330 DSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYS 378

Score = 135 bits (341), Expect = 1e-30
 Identities = 77/173 (44%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GTV+ +GI CQ W S PHEH +++ KDL+ENYCRNP G E P
 Sbjct: 305 CIQQGEGYRGTVNTIWNIGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 391 WCFTSNPEVRYEVCDDIPQCSEV---ECMTCNGESYRGLMDHTESGKICQRWDHQTTP--H 444
 WCFT++P +R C IP C +C NG++Y G + T SG C WD H
 Sbjct: 364 WCFTTDPNIRVGYSQIPNCDMSHGQDCYRNGKNYMGNLSQTRSGLTCSMWDKNMEDLH 423

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD ++NYCRNPD PWCYT +P W+YC I C +T
 Sbjct: 424 RHIFWE---PDASKLNENYCRNPDDAHGPWCYTGNPLIPWDYCPISRCEGDT 473

Score = 128 bits (322), Expect = 2e-28
 Identities = 75/175 (42%), Positives = 99/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRG+ T G+PCQ W ++P++H TP L EN+CRNPDG P
 Sbjct: 305 CIQQGEGYRGTVNTIWNIGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 126 WCYTTPDAVRFQSCG-IKSCREAA---CVWCNGEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ WD N H
 Sbjct: 364 WCFTTDPNIRVGYSQIPNCDMSHGQDCYRGNNGNYMGNLSQTRSGLTCSMWDKNMEDLH 423

Query: 180 NHPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTPDNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 424 RHIFWEPDA---SKLNENYCRNPDDDAHGPPWCYTGNPLIPWDYCPISRCEGDTTP 475

☐ >gi|226566|prf||1602237A hepatocyte growth factor [Rattus norvegicus]
 Length = 728

Score = 535 bits (1379), Expect = e-151
 Identities = 259/267 (97%), Positives = 261/267 (97%), Gaps = 5/267 (1%)

Query: 241 RKRRTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKA 300
 +KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRN GLPFTCKAFVFDKA
 Sbjct: 33 KKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNGLPFTCKAFVFDKA 92

Query: 301 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 360
 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW
 Sbjct: 93 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 152

Query: 361 SSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECM 415
 SSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECM
 Sbjct: 153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECM 212

Query: 416 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 475
 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY
 Sbjct: 213 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 272

Query: 476 TLDPHTRWEYCAIKTCADNTMNDTDVP 502
 TLDPHTRWEYCAIKTCADNT+NDTDVP
 Sbjct: 273 TLDPHTRWEYCAIKTCADNTVNDTDVP 299

Score = 242 bits (618), Expect = 9e-63
 Identities = 136/374 (36%), Positives = 191/374 (50%), Gaps = 38/374 (10%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E
 Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPDGGPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYRGAVDRTESGRECN 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R
 Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSERPWCYTTPDNIEREFCDLPRCGSEANP 232
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTVN 294

Query: 233 XXXXXXXXQKRRTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCA-----NRC 282
 + E + T+ P + ++ + D N C
 Sbjct: 295 DTDVPMETTECIQGQGEYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYC 354

Query: 283 TRNKGLPFTCKAFVFDKARK--QCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGK 340
 RN + F D + C P MS+G ++C G
 Sbjct: 355 -RNPDGSESPWCFTTDPNIRVGYSQIPNCDMSNG-----QDCYRGN 395

Query: 341 GRSYKGTVSITKSGIKCQPWSSMIP--HEHSYRGKDL---LQENYCRNPRGEEGGPWCFTS 395
 G++Y G +S T+SG+ C W+ + H H + D L ENYCRNP + GPWC+T
 Sbjct: 396 GKNYMGNLSQTRSGLTCSMWKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPPWCYTG 455

Query: 396 NPEVRYEVCDDIPQC 409
 NP + ++ C I +C
 Sbjct: 456 NPLIPWDYCPISRC 469

Score = 151 bits (381), Expect = 2e-35

Identities = 83/201 (41%), Positives = 104/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMTATTVGGLPCQAWSHKFPNDH 100
GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H

Sbjct: 186 GPWCFTSNPEVRYEVCDDIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGGPWCYTTPDAVRFQSCGIKSCRE----- 146
K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+C +

Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKTCADNTVNDTDVPMET 302

Query: 147 AACVWCNGEYRGAVDRTESGRECNRWDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSE 206
C+ GE YRG + +G C RWD +PH H P F L +NYCRNPDGSE

Sbjct: 303 TECIQQGEGYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSES 362

Query: 207 PWCYTTPDNIEREFCD-LPRC 226

PWC+TTDPNI +C +P C

Sbjct: 363 PWCFTTDPNIRVGYSQIPNC 383

Score = 140 bits (352), Expect = 6e-32

Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRNPRGEEGGP 390
C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P

Sbjct: 211 CMTCTNGESYRGLMDHTESGKICQRWDHQTTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 269

Query: 391 WCFTSNPEVRYEVCDDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
WC+T +P R+E C I C++ EC+ GE YRG + +G CQRW

Sbjct: 270 WCYTLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQQGEGYRGTTANTIWNGIPCQRW 329

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487

D Q PH+H PE + K +NYCRNPDG PWC+T DP+ R YC+

Sbjct: 330 DSQYPHKHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYS 378

Score = 131 bits (329), Expect = 3e-29

Identities = 74/173 (42%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGP 390
CI G+G Y+GT + +GI CQ W S PH+H +++ KDL+ENYCRNP G E P

Sbjct: 305 CIQQGEGYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 391 WCFTSNPEVRYEVCDDIPQC---SEVECMTCNGESYRGLMDHTESGKICQRWDHQTTP--H 444
WCFT++P +R C IP C + +C NG++Y G + T SG C W+ H

Sbjct: 364 WCFTTDPNIRVGYSQIPNCDMSNGQDCYRGNNGNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495

RH F PD ++NYCRNPD PWCYT +P W+YC I C +T

Sbjct: 424 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 473

Score = 125 bits (314), Expect = 1e-27

Identities = 74/175 (42%), Positives = 97/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMTATTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGGP 125
CI QG GYRG T G+PCQ W ++P+ H TP L EN+CRNPDG P

Sbjct: 305 CIQQGEGYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 126 WCYTTPDAVRFQSCG-IKSCREAA---CVWCNGEYRGAVDRTESGRECNRWDLNHP--H 179
WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ W+ N H

Sbjct: 364 WCFTTDPNIRVGYSQIPNCDMSNGQDCYRGNNGNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 180 NHPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTPDNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 424 RHIFWEPDA---SKLNEYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 475

☐ >gi|87647|pir||S06794 hepatocyte growth factor precursor (version 2) - human
 gi|32082|emb|CAA34387.1| (X16323) HGF (AA 1-728) [Homo sapiens]
 Length = 728

Score = 535 bits (1379), Expect = e-151
 Identities = 259/267 (97%), Positives = 261/267 (97%), Gaps = 5/267 (1%)

Query: 241 RKRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNGLPFTCKAFVFDKA 300
 +KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNGLPFTCKAFVFDKA
 Sbjct: 33 KKRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNGLPFTCKAFVFDKA 92

Query: 301 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 360
 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW
 Sbjct: 93 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 152

Query: 361 SSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECM 415
 SSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECM
 Sbjct: 153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECM 212

Query: 416 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 475
 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY
 Sbjct: 213 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 272

Query: 476 TLDPHTRWEYCAIKTCADNTMNDTDVP 502
 TLDPHTRWEYCAIKTCADNT+NDTDVP
 Sbjct: 273 TLDPHTRWEYCAIKTCADNTVNDTDVP 299

Score = 242 bits (618), Expect = 9e-63
 Identities = 136/374 (36%), Positives = 191/374 (50%), Gaps = 38/374 (10%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E
 Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NRCRNPDPGDPGGPWCYTTPDAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R
 Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSRPWCYTTPDNIEREFCDLPRCGSEANP 232
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTVN 294

Query: 233 XXXXXXXXQKRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCA-----NRC 282
 + E + T+ P + ++ + D N C
 Sbjct: 295 DTDVPMETTECIQGQGEYRGTA NTIWNIGPCQRWDSQYPHKHDMTPENFKCKDLRENYC 354

Query: 283 TRNKGLPFTCKAFVFDKARK--QCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGK 340
 RN + F D + C P MS+G ++C G
 Sbjct: 355 -RNPDGSESPWCFTTPDNIIRVGYSQIPNCDSNG-----QDCYRGN 395

Query: 341 GRSYKGTVSITKSGIKCQPWSSMIP--HEHSYRGKD--LQENYCRNPRGEEGGPWCFTS 395
 G++Y G +S T+SG+ C W+ + H H + D L ENYCRNP + GPWC+T
 Sbjct: 396 GKNYMGNLSQTRSGLTCSMWKNMEDLHRHIFWEPDASKLNEYCRNPDDDAHGPWCYTG 455

Query: 396 NPEVRYEVCDDIPQC 409
 NP + ++ C I +C
 Sbjct: 456 NPLIPWDYCPISRC 469

Score = 151 bits (381), Expect = 2e-35

Identities = 83/201 (41%), Positives = 104/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
 Sbjct: 186 GPWCFTSNPEVRYEVCDDIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGPGGPWCYTTPDAVRFQSCGIKSCRE----- 146
 K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+C +
 Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKTCADNTVNDTDVPMET 302

Query: 147 AACVWCNGEEYRGAVDRTESGRECNRWDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSE 206
 C+ GE YRG + +G C RWD +PH H P F L +NYCRNPDGSE
 Sbjct: 303 TECIQQGEGYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSES 362

Query: 207 PWCYTTPDNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P C
 Sbjct: 363 PWCFTTDPNIRVGYCSQIPNC 383

Score = 140 bits (352), Expect = 6e-32

Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
 Sbjct: 211 CMTCTNGESYRGLMDHTESGKICQRWDHQTTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 269

Query: 391 WCFTSNPEVRYEVCDDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
 WC+T +P R+E C I C++ EC+ GE YRG + +G CQRW
 Sbjct: 270 WCYTLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQGGEGYRGTTANTIWNGIPCQRW 329

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
 D Q PH+H PE + K +NYCRNPDG PWC+T DP+ R YC+
 Sbjct: 330 DSQYPHKHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCS 378

Score = 131 bits (329), Expect = 3e-29

Identities = 74/173 (42%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GT + +GI CQ W S PH+H +++ KDL+ENYCRNP G E P
 Sbjct: 305 CIQGGEGYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 391 WCFTSNPEVRYEVCDDIPQC---SEVECMTCNGESYRGLMDHTESGKICQRWDHQTTP--H 444
 WCFT++P +R C IP C + +C NG++Y G + T SG C W+ H
 Sbjct: 364 WCFTTDPNIRVGYCSQIPNCDMSNGQDCYRNGNGKNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD ++NYCRNPD PWCYT +P W+YC I C +T
 Sbjct: 424 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 473

Score = 125 bits (314), Expect = 1e-27

Identities = 74/175 (42%), Positives = 97/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRG T G+PCQ W ++P+ H TP L EN+CRNPDG P
 Sbjct: 305 CIQGGEGYRGTTANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 126 WCYTTPDAVRFQSCG-IKSCREAA---CVWCNGEEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ W+ N H
 Sbjct: 364 WCFTTDPNIRVGYCSQIPNCDMSNGQDCYRNGNGKNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 180 NHPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTPDNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 424 RHIFWEPDA---SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 475

☐ >gi|18490837|gb|AAH22308.1| (BC022308) Similar to hepatocyte growth factor (hep scatter factor) [Homo sapiens]
Length = 285

Score = 514 bits (1323), Expect = e-144
Identities = 252/252 (100%), Positives = 252/252 (100%)

Query: 240 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 299
QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
Sbjct: 32 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Query: 300 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
Sbjct: 92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPCSEVECMT CNG 419
WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPCSEVECMT CNG
Sbjct: 152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPCSEVECMT CNG 211

Query: 420 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 479
ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
Sbjct: 212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Query: 480 HTRWEYCAIKTC 491
HTRWEYCAIKTC
Sbjct: 272 HTRWEYCAIKTC 283

Score = 196 bits (498), Expect = 8e-49
Identities = 88/172 (51%), Positives = 115/172 (66%), Gaps = 3/172 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENF 114
E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H Y L+EN+
Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYRG---KDLQENY 171

Query: 115 CRNPDGDPGGPWCYTTPDAVRFQSCGIKSCREAAVCWNGEYRGAVDRTESGRECNRWD 174
CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C RWD
Sbjct: 172 CRNPRGEEGGPWCFTSNPEVRYEVC DIPCSEVECMT CNGESYRGLMDHTESGKICQRWD 231

Query: 175 LNHPHNHPFEPGKFLDNLDDNYCRNPDGSRPWCYTTPDNIEREFCDLPRC 226
PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
Sbjct: 232 HQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC 283

Score = 65.9 bits (159), Expect = 1e-09
Identities = 33/81 (40%), Positives = 44/81 (53%), Gaps = 6/81 (7%)

Query: 414 CMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 472
C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
Sbjct: 128 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRNPRGEEGGP 182

Query: 473 WCYTLDPHTRWEYCAIKTCAD 493
WC+T +P R+E C I C++
Sbjct: 183 WCFTSNPEVRYEVC DIPCSE 203

☐ >gi|2135339|pir||I59214 hepatocyte growth factor short form precursor - human
gi|32084|emb|CAA40802.1| (X57574) hepatocyte growth factor [Homo sapiens]
gi|184034|gb|AAA52649.1| (L02931) hepatocyte growth factor [Homo sapiens]
Length = 290

Score = 509 bits (1311), Expect = e-143
Identities = 252/257 (98%), Positives = 252/257 (98%), Gaps = 5/257 (1%)

Query: 240 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 299

Sbjct: 32 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Query: 300 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP

Sbjct: 92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC 414
 WSSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC

Sbjct: 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC 211

Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 474
 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC

Sbjct: 212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Query: 475 YTLDPHTRWEYCAIKTC 491
 YTLDPHTRWEYCAIKTC

Sbjct: 272 YTLDPHTRWEYCAIKTC 288

Score = 200 bits (509), Expect = 3e-50

Identities = 89/174 (51%), Positives = 118/174 (67%), Gaps = 2/174 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E

Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPGDPGGPWCYTTPDAVRFQSCGIKSCREAAVCWNGEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R

Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECMTNCGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSRPWCYTTPDNIEREFCDLPRC 226
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C

Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC 288

Score = 78.2 bits (191), Expect = 3e-13

Identities = 36/81 (44%), Positives = 47/81 (57%), Gaps = 1/81 (1%)

Query: 414 CMTNCGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 472
 C+ G SY+G + T+SG CQ W PH H FLP Y K +NYCRNP G+ P

Sbjct: 128 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGP 187

Query: 473 WCYTLDPHTRWEYCAIKTCAD 493
 WC+T +P R+E C I C++

Sbjct: 188 WCFTSNPEVRYEVCDDIPQCSE 208

☐ >gi|184030|gb|AAA35980.1| (M77227) competitive HGF antagonist [Homo sapiens]
 Length = 296

Score = 509 bits (1311), Expect = e-143

Identities = 252/261 (96%), Positives = 252/261 (96%), Gaps = 5/261 (1%)

Query: 240 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 299
 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK

Sbjct: 32 QKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Query: 300 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP

Sbjct: 92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC 414
 WSSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC

Sbjct: 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC 211

Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 474
 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
 Sbjct: 212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Query: 475 YTLDPHTRWEYCAIKTCADNT 495
 YTLDPHTRWEYCAIK D T
 Sbjct: 272 YTLDPHTRWEYCAIKNMRDIT 292

Score = 199 bits (506), Expect = 7e-50
 Identities = 88/169 (52%), Positives = 116/169 (68%), Gaps = 2/169 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E
 Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPGDPGGPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R
 Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVECMTNCGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSERPWCYTTPDNIEREFC 221
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C
 Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYC 283

Score = 76.6 bits (187), Expect = 8e-13
 Identities = 44/108 (40%), Positives = 57/108 (52%), Gaps = 8/108 (7%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
 Sbjct: 186 GPWCFTSNPEVRYEVC DIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCYTTPDAVRFQSCGIKSCRE 146
 K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+ R+
 Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKNMRD 290

Score = 76.3 bits (186), Expect = 1e-12
 Identities = 34/79 (43%), Positives = 46/79 (58%), Gaps = 1/79 (1%)

Query: 149 CVWCNGEYRGAVDRTESGRECNRWDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSE-RP 207
 C+ G Y+G V T+SG +C W PH H F P + L +NYCRNP G E P
 Sbjct: 128 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGP 187

Query: 208 WCYTTDPNIEREFCDLPRC 226
 WC+T++P + E CD+P+C
 Sbjct: 188 WCFTSNPEVRYEVC DIPQC 206

☐ >gi|12583697|dbj|BAB21499.1| (AB046610) hepatocyte growth factor HGF [Felis catu
 gi|22335679|dbj|BAC10545.1| (AB080187) hepatocyte growth factor [Felis catus]
 Length = 728

Score = 506 bits (1303), Expect = e-142
 Identities = 245/268 (91%), Positives = 253/268 (93%), Gaps = 5/268 (1%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKKVNTADQCANRCTRNKGLPFTCKAFVFDK 299
 Q+KRRNT+HEFKKSAKTTLIK DP LKIKTKK+NTADQCANRC RNKGLPFTCKAFVFDK
 Sbjct: 30 QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKKMTADQCANRCIRNKGLPFTCKAFVFDK 89

Query: 300 ARKQCLWFFPFSMSGKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARK+CLWFFPFSM+SGVKKEFGHEFDLYENKDYIRNCIIGK SYKGTVSITKSGIKCQP
 Sbjct: 90 ARKRCCLWFFPFSMTSGVKKEFGHEFDLYENKDYIRNCIIGKGSYKGTVSITKSGIKCQP 149

Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVEC 414
 W+SMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC DIPQCSEVEC

Sbjct: 150 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVEC 209

Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 474
MTCNGESYRG MDHTESGKICQRWD QTPHRHKFLPERYPDKGFDDNYCRNPDG+PRPWC

Sbjct: 210 MTCNGESYRGPMMDHTESGKICQRWDRQTTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 269

Query: 475 YTLDPHTRWEYCAIKTCADNTMNDTDVP 502
YTLDP T WEYCAIK CA +TMNDTDVP

Sbjct: 270 YTLDPDTPWEYCAIKMCAHSTMNDTDVP 297

Score = 203 bits (517), Expect = 4e-51
Identities = 88/175 (50%), Positives = 118/175 (67%), Gaps = 2/175 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ W+ P++H + P+ G L+E

Sbjct: 113 EFDLYENKDYIRNCIIGKGSYKGTVSITKSGIKCQPWNSMIPHEHSFLPSSYRGKDLQE 172

Query: 113 NFCRNPDPDGGPWCYTTPDAVRFQSCGIKSCREAAVCWNGEYRGAVDRTESGRECNR 172
N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R

Sbjct: 173 NYCRNPRGEEGGPWCFTSNPEVRYEVCDDIPQCSEVECMTNCGESYRGPMMDHTESGKICQR 232

Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSRPWCYTTPDNIEREFCDLPRCG 227
WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C

Sbjct: 233 WDRQTTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWCYTLPDTPWEYCAIKMCA 287

Score = 144 bits (363), Expect = 3e-33
Identities = 79/201 (39%), Positives = 103/201 (50%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMTTVGGLPCQAWSHKFPNDH 100
GPW E CD+ Q + C+ G YRG M T G CQ W + P+ H

Sbjct: 184 GPWCFTSNPEVRYEVCDDIPQCSEV--ECMTCNGESYRGPMMDHTESGKICQRWDRQTTPHRH 241

Query: 101 KYTPTL--RNGLEENFCRNPDPDGGPWCYTTPDAVRFQSCGIKSCREAA----- 148
K+ P G ++N+CRNPDG P PWCYT DP ++ C IK C +

Sbjct: 242 KFLPERYPDKGFDDNYCRNPDGKP-RPWCYTLPDTPWEYCAIKMCAHSTMNDTDVPMET 300

Query: 149 --CVWCNGEYRGAVDRTESGRECNRWDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSR 206
C+ GE YRG ++ +G C RWD +PH H P F L +N+CRNPDG+E

Sbjct: 301 TECIQQGEGYRGTINSIWNGVPCQRWDSQYPHQHDITPENFKCKDLRENFCRNPDGAES 360

Query: 207 PWCYTTPDNIEREFCD-LPRC 226
PWC+TTDPNI +C +P+C

Sbjct: 361 PWCFTTDPNIRVGYSQIPKC 381

Score = 136 bits (342), Expect = 9e-31
Identities = 68/169 (40%), Positives = 90/169 (53%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRNPRGEEGGP 390
C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P

Sbjct: 209 CMTNCGESYRGPMMDHTESGKICQRWDRQTTPHRHKFLPERYPDKGFDDNYCRNPDGKP-RP 267

Query: 391 WCFTSNPEVRYEVCDDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
WC+T +P+ +E C I C+ EC+ GE YRG ++ +G CQRW

Sbjct: 268 WCYTLPDTPWEYCAIKMCAHSTMNDTDVPMETTECIQGGEGYRGTINSIWNGVPCQRW 327

Query: 439 DHQTTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLPDTPHTRWEYCA 487
D Q PH+H PE + K +N+CRNPDG PWC+T DP+ R YC+

Sbjct: 328 DSQYPHQHDITPENFKCKDLRENFCRNPDGAESPWCFTTDPNIRVGYS 376

Score = 130 bits (327), Expect = 5e-29
Identities = 73/173 (42%), Positives = 98/173 (56%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GT++ +G+ CQ W S PH+H +++ KDL+EN+CRNP G E P
 Sbjct: 303 CIQGQGEYRGTTINSIWNGVPCQRWDSQYPHQHDITPENFKCKDLRENFCRNPDGAE-SP 361

Query: 391 WCFTSNPEVRYEVC-D-IPQC---SEVECMTNGESYRGLMDHTESGKICQRWDHQTTP--H 444
 WCFT++P +R C IP+C S +C NG++Y G + T SG C W+ H
 Sbjct: 362 WCFTTDPNIRVGYSQIPKCDVSSGQDCYRGNGKNYMGNLSKTRSGLTCSMWKCNMEDLH 421

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD + NYCRNP PWCYT +P W+YC I C +T
 Sbjct: 422 RHIFWE---PDASKLNKNYCRNPDDAHGPWCYTGNPLIPWDYCPISRCEGDT 471

Score = 125 bits (314), Expect = 1e-27
 Identities = 74/175 (42%), Positives = 97/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRG+ + G+PCQ W ++P+ H TP L ENFCRNPDPG P
 Sbjct: 303 CIQGQGEYRGTTINSIWNGVPCQRWDSQYPHQHDITPENFKCKDLRENFCRNPDGAE-SP 361

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA---CVWCNGEEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I C ++ C NG+ Y G + +T SG C+ W+ N H
 Sbjct: 362 WCFTTDPNIRVGYSQIPKCDVSSGQDCYRGNGKNYMGNLSKTRSGLTCSMWKCNMEDLH 421

Query: 180 NHPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTPDNIEREFCDLPRCGSEANP 232
 H F EP + L+ NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 422 RHIFWEPDA---SKLNKNYCRNPDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 473

☐ >gi|220438|dbj|BAA01065.1| (D10213) hepatocyte growth factor precursor [Mus mus
 Length = 723

Score = 493 bits (1269), Expect = e-138
 Identities = 234/263 (88%), Positives = 247/263 (92%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCRTRNKGLPFTCKAFVFDK 299
 Q+KRRNT+HEFKKSAKTTL K DP LKIKTKKVNTAD+CANRC RN+G FTCKAFVFDK
 Sbjct: 33 QKKRRNTLHEFKKSAKTTLTKEPDLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Query: 300 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 +RK+C W+PFNSMSSGVKK FGHEFDLYENKDYIRNCIIGKG SYKGTVSITKSGIKCQP
 Sbjct: 93 SRKRCYWYFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGSYKGTVSITKSGIKCQP 152

Query: 360 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC-D-IPQCSEVECMTNG 419
 W+SMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC-D-IPQCSEVECMTNG
 Sbjct: 153 WNSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVC-D-IPQCSEVECMTNG 212

Query: 420 ESYRGLMDHTESGKICQRWDHQTTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 479
 ESYRG MDHTESGK CQRWD QTPHRHKFLPERYPDKGFDDNYCRNPDG+PRPWCYTLDP
 Sbjct: 213 ESYRGPMDDHTESGKTCQRWDQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWCYTLDP 272

Query: 480 HTRWEYCAIKTCADNTMNDTDVP 502
 T WEYCAIKTCA + +N+TDVP
 Sbjct: 273 DTPWEYCAIKTCAHSAVNETDVP 295

Score = 238 bits (606), Expect = 2e-61
 Identities = 135/372 (36%), Positives = 187/372 (49%), Gaps = 39/372 (10%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENF 114
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ W+ P++H Y L+EN+
 Sbjct: 116 EFDLYENKDYIRNCIIGKGSYKGTVSITKSGIKCQPWNSMIPHEHSYRG---KDLQENY 172

Query: 115 CRNPDGDPGGPWCYTTPDPAVRFQSCGIKSCREAAACVWCNGEEYRGAVDRTESGRECNRW 174
 CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C RWD